

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 3, 2002, 22:53:44 ; Search time 33.32 Seconds  
(without alignments)  
2110.117 Million cell updates/sec

Title: US-09-497-822a-19  
Perfect score: 4912  
Sequence: 1 MEVOLGLGRVPRPPSKTYR.....SVQPKILSGKVKPIYFHTQ 923

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4880	99.3	919	2 A39248	androgen receptor
2	4798.5	97.7	910	2 A34721	androgen receptor
3	4763	97.0	911	2 B34721	androgen receptor
4	4206.5	85.6	902	2 B40494	androgen receptor
5	4176	85.0	899	2 A35895	androgen receptor
6	1676	34.1	344	2 I51330	androgen receptor
7	1523	31.0	848	2 JG0194	androgen receptor
8	1262.5	25.7	930	2 A25923	progesterone recep
9	1262	25.7	933	1 QRHUP	progesterone recep
10	1234	25.1	923	2 I53280	progesterone recep
11	1218	24.8	786	2 A35466	progesterone recep
12	1205	24.5	923	2 A39596	progesterone recep
13	1092	22.2	981	2 A31401	progesterone recep
14	1078.5	22.0	984	2 A29513	mineralocorticoid
15	1065	21.7	795	1 QRRTG	glucocorticoid rec
16	1063.5	21.7	783	1 A25691	glucocorticoid rec
17	1054.5	21.5	776	1 S44047	glucocorticoid rec
18	1042	21.2	777	1 QRHUGA	glucocorticoid rec
19	1023	20.8	758	2 S60586	glucocorticoid rec
20	1003	20.4	771	2 A54273	glucocorticoid rec
21	943.5	19.2	742	1 QRHUGB	glucocorticoid rec
22	715	14.6	166	2 S35795	estradiol receptor
23	502	10.2	595	2 I47140	estrogen receptor
24	491	10.0	586	1 ORXLE	estrogen receptor
25	485.5	9.9	600	1 ORRTE	estrogen receptor
26	478	9.7	595	1 QRHUE	80K estrogen recep
27	478	9.7	701	2 S64737	estrogen receptor
28	474	9.6	589	1 QRCHC	estrogen receptor
29	474	9.6	599	1 QRMSE	estrogen receptor

30 461.5 9.4 620 2 T10423  
31 448 9.1 535 2 S58224  
32 444 9.0 574 2 A37197  
33 442 9.0 503 2 JW0046  
34 437.5 8.9 477 2 S71400  
35 437.5 8.9 530 2 JC5939  
36 398.5 8.1 1043 2 T13733  
37 391 8.0 433 2 S58087  
38 387.5 7.9 433 2 B29345  
39 383 7.8 521 2 A29345  
40 379 7.7 462 2 S44490  
41 370.5 7.5 543 2 A32693  
42 364.5 7.4 746 2 B32693  
43 357 7.3 533 2 S37781  
44 346 7.0 422 2 I48305  
45 343.5 7.0 423 2 S02710

## ALIGNMENTS

RESULT 1  
A39248  
androgen receptor - human  
C:Species: Homo sapiens (man)  
C>Date: 04-Oct-1991 #sequence\_revision 04-Oct-1991 #text\_change 24-Nov-1999  
R:Accession: A39248; A30328; A40109; A60946; A34942; A27653; A40108; A40494; A32224;  
R:Lubahn, D.B.; Brown, T.R.; Simental, J.A.; Higgins, H.N.; Migeon, C.J.; Wilson, E.M.;  
Proc. Natl. Acad. Sci. U.S.A. 86, 9534-9538, 1989  
A>Title: Sequence of the intron/exon junctions of the coding region of the human andr  
A:Reference number: A39248; MUID:90083302  
A:Accession: A39248  
A:Molecule type: DNA  
A:Residues: 1-919 <LUB>  
A:Cross-references: GB:M27423; GB:M27430; NID:g178904; PIDN:AAA51886.1; PID:g178906  
R:Faber, P.W.; Kuiper, G.G.J.M.; van Rooij, H.C.J.; van der Korput, J.A.G.M.; Brinkma  
Mol. Cell. Endocrinol. 61, 257-262, (1989)  
A>Title: The N-terminal domain of the human androgen receptor is encoded by one, larg  
A:Reference number: A30328; MUID:89137730  
A:Accession: A30328  
A:Molecule type: DNA  
A:Residues: 1-77,79-165, 'A', 167-389, 'L', 391-464, 473-538 <FAB>  
A:Cross-references: GB:M20260  
R:Lubahn, D.B.; Joseph, D.R.; Sullivan, P.M.; Willard, H.F.; French, F.S.; Wilson, E.  
Science 240, 327-330, (1988)  
A>Title: Cloning of human androgen receptor complementary DNA and localization to the  
A:Reference number: A40109; MUID:88178112  
A:Accession: A40109  
A:Molecule type: DNA  
A:Residues: 559-624 <LU2>  
A:Cross-references: GB:M20132  
R:Kuiper, G.G.J.M.; Faber, P.W.; van Rooij, H.C.J.; van der Korput, J.A.G.M.; Ris-Sta  
J. Mol. Endocrinol. 2, 1265-1275, (1988)  
A>Title: Structural organization of the human androgen receptor gene.  
A:Reference number: A60946; MUID:89322749  
A:Accession: A60946  
A:Molecule type: DNA  
A:Residues: 536-540  
R:Lubahn, D.B.; Joseph, D.R.; Tan, J.; Higgs, H.N.; Larson, R.E.; French, F.  
Mol. Endocrinol. 2, 1265-1275, (1988)  
A>Title: The human androgen receptor, complementary deoxyribonucleic acid cloning, se  
A:Reference number: A34942; MUID:89112208  
A:Accession: A34942  
A:Molecule type: mRNA  
A:Residues: 1-919 <LU3>  
A:Cross-references: GB:M20132; NID:g178627; PIDN:AAA51729.1; PID:g178628; GB:J03180  
R:Trapman, J.; Klaassen, P.; Kuiper, G.G.J.M.; van der Korput, J.A.G.M.; Faber, P.W.;  
Biochem. Biophys. Res. Commun. 153, 241-248, (1988)  
A>Title: Cloning, structure and expression of a cDNA encoding the human androgen rece  
A:Reference number: A27653; MUID:88240407  
A:Accession: A27653  
A:Molecule type: mRNA  
A:Residues: 468-564, 'K', 566-919 <TRA>





Db 888 AEIISVQVPKILSGKVPIFHTQ 911

RESULT 4  
B40494  
androgen receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 20-Sep-1999  
C:Accession: B40494; A34943; A36283; B40108  
R:Chang, C.; Kokontis, J.; Liao, S.  
Proc. Natl. Acad. Sci. U.S.A. 85, 7211-7215, 1988  
A>Title: Structural analysis of complementary DNA and amino acid sequences of human and  
A:Reference number: A40494; WUID:89017168  
A:Accession: B40494  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-902 <CHA>  
A:Cross-references: GB:M20133; NID:g202895; PIDN:AAA40733.1; PID:g202968  
R:Tan, J.; Joseph, D.R.; Quarmby, V.E.; Lubahn, D.B.; Sar, M.; French, F.S.; Wilson, E.M.  
Mol. Endocrinol. 2, 1276-1285, 1988  
A>Title: The rat androgen receptor: primary structure, autoregulation of its messenger RNA  
A:Reference number: A34943; WUID:89112209  
A:Accession: A34943  
A:Molecule type: mRNA  
A:Residues: 1-388,'S',390-902 <TAN>  
A:Cross-references: GB:M20133; NID:g202895; PIDN:AAA40733.1; PID:g202896  
R:Yarborough, W.G.; Quarmby, V.E.; Simental, J.A.; Joseph, D.R.; Sar, M.; Lubahn, D.B.; C  
J. Biol. Chem. 265, 8893-8900, 1990  
A>Title: A single base mutation in the androgen receptor gene causes androgen insensitivity  
A:Reference number: A36283; WUID:90256822  
A:Accession: A36283  
A:Molecule type: mRNA  
A:Residues: 1-194,196-902 <YAR>  
A:Cross-references: GB:J05454  
R:Chang, C.; Kokontis, J.; Liao, S.  
Science 240, 324-326, 1988  
A>Title: Molecular cloning of human and rat complementary DNA encoding androgen receptor  
A:Reference number: A40108; WUID:88178111  
A:Accession: B40108  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 540-611 <CH2>  
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
C:Keywords: DNA binding; zinc finger  
F:540-798/Domain: erba transforming protein homology <ERBA>  
F:542-562/Region: zinc finger  
F:578-602/Region: zinc finger

Query Match 85.6%; Score 4206.5; DB 2; Length 902;  
Best Local Similarity 84.7%; Pred. No. 5.2e-215; Indels 57; Gaps 4;  
Matches 797; Conservative 36; Mismatches 51;

Qy 1 MEVOLGLGRVYPRPSKTYRGAFQNLFOSVREVIONPGRPHEASAAPPGASLLLLQQQ 60  
Db 1 MEVOLGLGRVYPRPSKTYRGAFQNLFOSVREAIQNPGRPHEAASTAPPGACL----- 54  
Qy 61 QQQ 119  
Db 55 -----QQ 96  
Qy 120 QPQSALCEHPERGCVPEPCGAVAASKGLPQQLPAPPPDEDDSAAPSTLSLLGPTFFGLSSC 179  
Db 97 QQQSASEGPESGCLPEPCAATAPCKGLPQQPPAPDPDQDSAAPSTLSLLGPTFFGLSSC 156  
Qy 180 SADLKDILEASETMOLL-----QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 222  
Db 157 SADIKDILEAGTMQLLQOQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 216  
Qy 223 SKDNLYGGNSTSDNAKELCAVSVSMGLGVLEHLSPGEOLRGDCMYAPILLGVPPAVR 282  
Db 217 SKDYSYGGNSTSDNAKELCAVSVSMGLGVLEHLSPGEOLRGDCMYASLLGGPPAVR 276

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A:Accession: A37908
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-899 <CHA>
A:Cross-references: GB:S56585; NID:q236048; PIDN:AA819916.1; PID:q236049
R:Faber, P.W.; King, A.; van Rooij, H.C.J.; Brinkmann, A.O.; de Both, N.J.; Trapman, J.
Biochem. J. 278, 269-278, 1991
A:Title: The mouse androgen receptor. Functional analysis of the protein and characterization
A:Reference number: S17198; MUID:91354214
A:Accession: S34398
A:Molecule type: DNA
A:Residues: 1-899 <FAB>
A:Cross-references: EMBL:X59592; NID:g49968; PIDN:CAA42160.1; PID:g49969
A:Accession: S17198
A:Molecule type: mRNA
A:Residues: 1-899 <FA2>
A:Cross-references: GB:X59592; NID:g49968; PIDN:CAA42160.1; PID:g49969
R:He, W.W.; Kumar, M.V.; Findall, D.J.
Nucleic Acids Res. 19, 2373-2378, 1991
A:Title: A frame-shift mutation in the androgen receptor gene causes complete androgen
A:Reference number: S40626; MUID:91252278
A:Accession: S40626
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 366-413 <HEW>
A:Cross-references: EMBL:X53779
R:Gaspar, M.
Proc. Natl. Acad. Sci. U.S.A. 88, 8606-8610, 1991
A:Title: A single base deletion in the Tfm androgen receptor gene creates a short-lived
A:Reference number: I49501; MUID:92020902
A:Accession: I49501
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-899 <RES>
A:Cross-references: GB:M37890; NID:g191935; PIDN:AAA37234.1; PID:g191936
C:Genetics:
A:Introns: 518/2; 569/1; 704/1; 752/2; 796/1; 848/3
A:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; transcription regulation; zinc finger
F:1-536/Domain: regulatory status predicted <REG>
F:537-795/Domain: regulatory status predicted <REG>
F:539-559/Region: zinc finger
F:575-599/Region: zinc finger
F:650-899/Domain: hormone binding #status predicted <LIG>

Query Match 85.0%; Score 4176; DB 2; Length 899;
Best Local Similarity 84.1%; Pred. No. 2.1e-213;
Matches 790; Conservative 40; Mismatches 53; Indels 56; Gaps 5;

QY 1 MEVQLGLGRVYPRPSKTYRGAFONLFQSVREVTONFGPRHPEAASAPPGASLLILQQQ 60
Db 1 MEVQLGLGRVYPRPSKTYRGAFONLFQSVREATONFGPRHPEAANTAPPGACL----- 54

QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 119
Db 55 -----QQQQTSPRRRRQQHTEDGSGQAHLIRGPTGYLALAEQQQPS 96

QY 120 QPQSALECHPERGCVPEGAANAASKGLPQOLPAPPPEDDSDAAPTSLSLGPTFPGLSSC 179
Db 97 QQQAAASEGHPESSCLPEGAATAPKGLPQPPAPPDQDSDAAPTSLSLGPTFPGLSSC 156

QY 180 SADKLILSEASTMQLIQ-----QQQQAQVSESSSGRAREASGAPTSK 224
Db 157 SADIKDILNEAGTWQLLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 215

QY 225 DNYLGSTTISDNKAEKCAVSMGLGVLEALHSLSPGEOLRGDCMYAPLLGVPPAVRPT 284
Db 216 DSYLGNSTISDSAKELCAVSMGLGVLEALHSLSPGEOLRGDCMYASLLGGPFAVRPT 275

QY 285 PCAPLAECKGLLDDSAKSTEDTAESYSPFKGGTYTGKLEGESLGCSSGAAGSSGTTLEP 344
Db 276 PCAPLECKGLPLDEGPGKSTETAESYSPFKGGYAKLEGESLGCSSGAAGSSGTTLEP 335

345 STLSLYKSGALDEAAAVQSDRYNFPALALAGPPPPPPPPHARIKLENPLDYGSAWAAA 404
Db 336 STLSLYKSGALDEAAAYQNDYYNFPALUSGPPPPPPHARIKLENPLDYGSAWAAA 395
QY 405 AACRCYGDLSAFHGAGAAGPGSGSPASAAASSSWHTLFTAEEOQLYGPCGGGGGGGGGG 464
Db 396 AACRCYGDLSLHGGSVAGPSTGSPATTSWHTLFTAEEOQLYGP----- 442
QY 465 GGGGGGGGGGAGAVADYGYTRPPQGLAGQESDFTADVWYPGGMVSRVYPSPTCVK 524
Db 443 --GGGGSSSPDAGPVADYGYTRPPQGLTSOESDYSASEVWYPGGVNVRVYPSPCVK 500
QY 525 SEMGPWMDSYSGPYGDMRLTARDHVLPIIDYFFPQKTCILCGDEASGCHYGALTCGSK 584
Db 501 SEMGPWENYSGPYGDMRLDSTRDHVLPIDYFFPQKTCILCGDEASGCHYGALTCGSK 560
QY 585 VPFKRAAEGKQYLACASRNDCTIDFRKNCPCSLRKYEAGMTLGARKLKLGNLKLQ 644
Db 561 VPFKRAAEGKQYLACASRNDCTIDFRKNCPCSLRKYEAGMTLGARKLKLGNLKLQ 620
QY 645 EGEASSTTSPTTEETQKLTVSHIEGYEQPIFLNVLEAIEPGVVCAGHDNNQDPSAAL 704
Db 621 EGENSNAGSPTEDPSQKMTVSHIEGYEQPIFLNVLEAIEPGVVCAGHDNNQDPSAAL 680
QY 705 LSLNELGERQLVHVVKWAKALPGFRNLHVDQMAVIOYSWMGLMVFAMGWSFTNVNSR 764
Db 681 LSLNELGERQLVHVVKWAKALPGFRNLHVDQMAVIOYSWMGLMVFAMGWSFTNVNSR 740
QY 765 MLYFAPDLVFNRYMHKSRMYSQCVRMHRLSQEFGWGLQITPQEFCLMKALLFSIIPVDG 824
Db 741 MLYFAPDLVFNRYMHKSRMYSQCVRMHRLSQEFGWGLQITPQEFCLMKALLFSIIPVDG 800
QY 825 LKNQKFFDELRMNYIKELDRIIACKRNKPTSCSRFFQYLTKLDSVOPIARELHQFTFDL 884
Db 801 LKNQKFFDELRMNYIKELDRIIACKRNKPTSCSRFFQYLTKLDSVOPIARELHQFTFDL 860
QY 885 LKSHMWSVDFPEMMAEIIISVQVFKILSGKVKPIYFHTQ 923
Db 861 LKSHMWSVDFPEMMAEIIISVQVFKILSGKVKPIYFHTQ 899

RESULT 6
I51330
androgen receptor - common canary (fragment)
C:Species: Serinus canaria (common canary)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Sep-1999
C:Accession: I51330
R:Nastiuk, K.L.; Clayton, D.F.
Endocrinology 134, 640-649, 1994
A:Title: Seasonal and tissue-specific regulation of canary androgen receptor message
A:Reference number: I51330; MUID:94130808
A:Accession: I51330
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-344 <NAS>
A:Cross-references: GB:I25901; NID:g414733; PIDN:AAAI7402.1; PID:g414734
C:Genetics:
A:Gene: AR
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: zinc finger
F:1-251/Domain: erba transforming protein homology (fragment) <ERBA>

Query Match 34.1%; Score 1676; DB 2; Length 344;
Best Local Similarity 90.4%; Pred. No. 9.1e-82;
Matches 311; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 569 EASGCHYGALTCGSKVFFKRAAEGKQYLACASRNDCTIDFRKNCPCSLRKYEAGM 628
Db 1 EASGCHYGALTCGSKVFFKRAAEGKQYLACASRNDCTIDFRKNCPCSLRKYEAGM 60
QY 629 TLGARKLKLGNLKLQEGEASSTTSPTTEETQKLTVSHIEGYEQPIFLNVLEAIEPGV 688
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Db 61 TLGARKLKLGNLKAQDDIEGASSSSPTTEQAPKLVMTRIDGYECQIFLVNLEAIEPGV 120  
Qy 689 VCAGHDNNQPDSSFAALLSSINELGERQLVHVVKWAKALPGPRNLHVDQMAVIOYSWMGL 748  
Db 121 VCAGHDNSQDSSFNLLTSLNELGERQLVHVVKWAKALPGPRNLHVDQMSIIQYSWMGL 180  
Qy 749 MVFAMGWRSTNVSRLMYFAPDLVFNEMHKSRLMYSCQVVRHLSQEFQWGLQITPOEF 808  
Db 181 MVFAMGWRSTNVSRLMYFAPDLVFNEMHKSRLMYSCQVVRHLSQEFQWGLQITPOGF 240  
Qy 809 LCMKALLFSIIPVDGLKKNQKFFDELRLMYIKELDRITACKRKNPTSCSRREYQITKLID 868  
Db 241 LCMKALLFSIIPVDGLKKNQKFFDELRLMYIKELDRITACKRKNPTSCSRREYQITKLID 300  
Qy 869 SVOPIARELHQFTFDLLIKSHMYSVDPEPMAELIISVQVPKILS 912  
Db 301 SVTPIAKDLHQFTFDLLIKAHMYSVDPEPMAELIISVQVPKILS 344  
RESULT 7  
JG0194  
androgen receptor - Japanese eel  
C:Species: Anguilla japonica (Japanese eel)  
C:Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 11-May-2000  
C:Accession: JG0194  
R:Todo, T.; Ikeuchi, T.; Kobayashi, T.; Nagahama, Y.  
Biochem. Biophys. Res. Commun. 254, 378-383, 1999  
A:Title: Fish androgen receptor: cDNA cloning, steroid activation of transcription in the  
A:Reference number: JG0194; MUID:99119319  
A:Accession: JG0194  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-848 <TOD>  
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
F:491-745/Domain: erba transforming protein homology <ERB>

Query Match 31.0%; Score 1523; DB 2: Length 848;  
Best Local Similarity 37.5%; Pred. No. 3e-73;  
Matches 380; Conservative 118; Mismatches 258; Indels 256; Gaps 31:

Qy 1 MEVQGLGRVYPRPSKTYRGAFAQNLFSQSVREVIONPGPRHPEAASAPPGASLLLLQQQ 60  
Db 1 METPVLGLGV-SDATNAVFRGPYQNVFHSLOVAFQSHG---AVSRSLDFTNTYGFQVLRN 56  
Qy 61 QQQ 111  
Db 57 HFCMRQENKQ-----PPCKGLGLFYGNHRNSDTG--T 87  
Qy 112 LDEEQSQPOQSALECHPERGCVPEPAAVAASKGLPQOLPAPPDEDDSAAPSTLSLLGP 171  
Db 88 NEDDTIACFRSQSDAEA-----RPGLFSSSLDTGDEITCKLQSDNQGVAS---GP 135  
Qy 172 TFPGLSSCADLKILSEASTMQLLQOQQQPAVSEGGSSGRARASGAPTSSKDNLYLGGT 231  
Db 136 LLPGSGCNSGKSSSLACTS-----QORETTSQSDT-----CAGESCSSEHO-----A 177  
Qy 232 STTSDNAKELCAVSVSMGLVGEALHLSLPGELRGDCMYAPLLGVPAVRPTCAPLAE 291  
Db 178 TTISTARELCNANVSVSLGNDLND-----  
Qy 292 CKGSLDDDSAGKSTETA-----EYSPFKGGYT-KGLEGESLCCSGSAAGSGGTLELP 344  
Db 204 -MNDLSNIOISSTESTSOAIYLFESSP---GYTCVGLNALVRDCKQCSAREGTSTQO-- 257  
Qy 345 STLKSLYSGALDEAAAYQSRDYNTPLAGPPPPPPPPHARIKLENPLDYGSAW--- 401  
Db 258 -----YDRGAM-----FKINRVNDLPLOQAPPRTTSTIS-----DAKWDME 292  
Qy 402 AAAAAQCRVGD---LASLHCGAA--  
Db 293 AGLCAQMEHKDSEKCANMDGAHSTSVFSQFQELLPVNASHYSONVSVRVEPQSDFSPILY 352

Qy 423 -GPGSGSPSAAASSSWHTLFTAEGOLYPCGGGGGGGGGGGGGGGGGGGGGGGGG 481  
Db 353 KSPGIQKNAEKYNVOIDATIKSEDKTTSEREWG-----  
Qy 482 APYGY-----TRPPOGLAQ-----ESDFTAPDVVYPGMVSRVPY----- 517  
Db 387 FOYRYNESCSSTSPAPRHCAHQNRAGPYNQFFNPFYAKRGVSVREGYSLEHGFNNLA 446  
Qy 518 --PSPTCVKSEGMWDSYSGPYGDM--RLETARDHVLPIDYFPPKPTCLICGDEASGC 573  
Db 447 RTPYSGSLKNELG---DRLSGPYPDVSVRYEGEENVEFVFPPTQPTCLICGDEASGC 503  
Qy 574 HYGALTCGCKGVFFKRAABGKOKYLCASRNDCTIDKFRKNCPCRLRCKEYAGMTLGR 633  
Db 504 HYGALTCGCKGVFFKRAABGKOKYLCASINDCTIDKRRKNCPCRLRCKFAAGMTLGR 563  
Qy 634 KLKKLGNLKLQEBGEASSTTSPTETTKLVIS--HIEGYECQIFLVNLEAIEPGVYVCA 691  
Db 564 KLKKIQMRAPEDGQ---GPAE---AELSVSPKYDLGFTQSMFLNLEAIEPEVVNA 617  
Qy 692 GHNNQPDSSFAALLSSINELGERQLVHVVKWAKALPGPRNLHVDQMAVIOYSWMGLMV 751  
Db 618 GHYQGPDSASLTLTSLNELGERQLVHVVKWAKALPGPRSLYVDQMTVIQKHMAVMVF 677  
Qy 752 AMGWRSTNVSRLMYFAPDLVFNEMHKSRLMYSCQVVRHLSQEFQWGLQITPOEFQV 811  
Db 678 ALGWRSEKKNVKSRLMYFAPDLVFNEMHKSRLMYSCQVVRHLSQEFQWGLQITPOEF 737  
Qy 812 KALLFSIIPVDGLKKNQKFFDELRLMYIKELDRITACKRKNPTSCSRREYQITKLIDSVQ 871  
Db 738 KALLFSIIPVDGLKKNQKFFDELRLMYIKELDRITACKRKNPTSCSRREYQITKLIDSVQ 795  
Qy 872 PIARELHQFTFDLLIKSHMYS--VDFPEMMAELISVQVPKILSGVKVPYF 921  
Db 796 PVLKKLHQFTFDLVQSONLSNQVCEPMEISELISVHVVKILAGTVKPIPLH 847  
RESULT 8  
A25923  
progesterone receptor - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 20-Aug-1999  
C:Accession: A25923  
R:Loosfelt, H.; Atger, M.; Misrahi, M.; Guiochon-Mantel, A.; Meriel, C.; Logeat, F.;  
Proc. Natl. Acad. Sci. U.S.A. 83, 9045-9049, 1986  
A:Title: Cloning and sequence analysis of rabbit progesterone-receptor complementary  
A:Reference number: A25923; MUID:87067449  
A:Accession: A25923  
A:Molecule type: mRNA  
A:Residues: 1-930 <100>  
C:Cross-references: GB:M14547; NID:gl165631; PIDN:AAA31443.1; PID:gl165632  
C:Superfamily: progesterone receptor; erba transforming protein homology  
C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation;  
F:566-826/Domain: erba transforming protein homology <ERBA>  
F:568-588/Region: zinc finger  
F:604-628/Region: zinc finger

Query Match 25.7%; Score 1262.5; DB 2: Length 930;  
Best Local Similarity 33.8%; Pred. No. 2e-59;  
Matches 336; Conservative 122; Mismatches 308; Indels 227; Gaps 31:

Qy 1 MEVQGLGRVYPRPSKTYRGAFAQNLFSQSVREVIONP-----G 38  
Db 91 VEAPEAGDSSSRPEKD-----SGLDSDVLTDTLAFSGGQSHASPATCEAISPWCLFG 145  
Qy 39 PRUPEAASAPPGASLLLLQOQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 98  
Db 146 PDLPEPRAAPATKGVL-----APLMSRPEDRAGDSSGT 179  
Qy 99 PQAHR---RG---PTGYLVLDDEQQPSQPSQSALECHPERGCVPEPAAVAASKGLPQOLPA 153



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QY 459 GGGGGGGGGGGGGEAGAVAPYTRPPGOLAGQESDFTAPDVWPGMVSR-VPY 517
Db 486 SGCLLPDRGLPSTASAAAAGA-APALY--PALGLNG-----LPQGYOAAVLKESGLQ 536
QY 518 PSPTCVKSEKMPWMDSYSGPYGDMRLTARDHVLPIIDYPP--PQKTCICGDEASGCHY 575
Db 537 VYPPYL-NYLRPDSEASQSP-----QYSESLPQKTCICGDEASGCHY 579
QY 576 GALTGCGCKVFFKRAAGKOKYLACSRNDCTIDKFRKNCPSRLRKCYEAGMTLGARKL 635
Db 580 GVLTCGCGKVFVRKAMEGQNHLYCAGNRDCLVDKIRKNCPCALRKCQAGMVLGGRKF 639
QY 636 KKLGNLKLQEEGEASSTSP-----TEETQKLTVSHIEGYEQPIFLNVLEAIEPGVV 689
Db 640 KFKNVVRVRAIDAVLPQPLGVNPSQALSQRFTFPGQDIOILPPLINLLMSIEPDVI 699
QY 690 CAGHNDNQPDSFAALLSLNELGERQLVHVWVKAKALPGFRNLHVDDOMAVIOYSWGLM 749
Db 700 YAGHDNTKPDTSLSLLTSLNOLGERQLVHVWVKSLPGFRNLHIDQIITLIQISWLSM 759
QY 750 VFAMGWRSTFNVNMLYFAPDLVFNVRHKSRYSCQVVRHLSQEFGLWLTITPQEF 809
Db 760 VEGWRSYKIVSQMQLYFAPDLILNEORMKESFYSLCTMWCIPQEFVKLVQVSEFL 819
QY 810 CMKALLFSIIPVGLKNQKFFDELWNYIKELDRITACKRNKPTSCRRFYQLTKLDS 869
Db 820 CMKVLLENTIPLGLRSQTOFEEMRSYIRELIKAIGLQKQGVVSSORFYQLTKLND 879
QY 870 VOPIARELHQFTDLLIKSHMVSVDFPEMMAEIIISVQVPKILSCGVKPIYFH 921
Db 880 LHDVLQHLQLCLNTFIQSRLSVFEPFEMSEVIAAQLPKILAGMVKPLLFH 931

RESULT 10
I53280
progesterone receptor B form - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: I53280; B23733; A49574; A23733
R:Park, O.K.; Mayo, K.E.
Endocrinology 134, 709-718, 1994
A:Title: Regulation of the progesterone receptor gene by gonadotropins and cyclic adenosine
A:Reference number: I53280; MUID:94130817
A:Accession: I53280
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-923 <PAR1>
A:Cross-references: GB:L16922; NID:g463282; PIDN:AAA19916.1; PID:g463283
R:Park, O.K.; Mayo, K.E.
Mol. Endocrinol. 5, 967-978, 1991
A:Title: Transient expression of progesterone receptor messenger RNA in ovarian granulosa
A:Reference number: A23733; MUID:92049379
A:Accession: B23733
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 555-589, 'W', 591-624, 742-910 <PAR2>
A:Cross-references: GB:S64044
R:Kraus, W.L.; Montano, M.M.; Katzenellenbogen, B.S.
Mol. Endocrinol. 7, 1603-1616, 1993
A:Title: Cloning of the rat progesterone receptor gene 5'-region and identification of t
A:Reference number: A49574; MUID:94195318
A:Accession: A49574
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <KRA>
A:Cross-references: GB:S69361; NID:g546178
C:Superfamily: progesterone receptor; erba transforming protein homology
C:Keywords: DNA binding; nucleus; steroid hormone receptor; zinc finger
F:555-819/Domain: erba transforming protein homology <ERBA>
F:557-577/Region: zinc finger
F:593-617/Region: zinc finger

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Query Match 25.18; Score 1234; DB 2; Length 923;
Best Local Similarity 33.18; Pred. No. 6.3e-58;
Matches 344; Conservative 129; Mismatches 269; Indels 266; Gaps 39;

QY 15 PSKTYRGA-----FQNLFSQSVREVIONPGPRHPEAASAAAPP-----GASLLLLLOQQQ 61
Db 19 PSPTWVGSPLLARLDPDFQ-----GSHSDASSVVSPISLDRLLEFSRSC 65
QY 62 QQQQQQQQQQQQQQQQ-----QQQQQQQETSPROQQQQQGGEDGSPQARRGPTCYL 110
Db 66 QQAELPDEKTONQOQSLSDVEGAFSGVEASRRRRSRNPRAPKEDSRLLDS----- 113
QY 111 VLDEEQQSPQOSALECHPERGC-----VPEPGAUAASKGLPOOLPAPPDE- 157
Db 114 VLDTLLAPSGPEQSOTSPP--ACEAITSWCLFPGPELPEPRSVKATKLLSPLMSRPSK 171
QY 158 --DSSAA-----PSTLS-----LLGPTF-----PGLSSCSADLKD---ILSEA 190
Db 172 AGDSSGTGAGQKVLKAVSPPRQLLPTSGSAHWPGAGVKPSQQPATVEVEDGGLETEG 231
QY 191 STMQLLQQQQQEAIVSEGGSSGRARASGAPTSSKDNYLGGTSTI-SDNAKELCKAVSYSM 249
Db 232 SAGPLLKSKPRALEGCMCGGGVTANAPGAAP-----GGVTLVPKEDSRFSAPRVSLQ 284
QY 250 GLGV-----EALHLSPEQQLRGDCM-----YAPLLGV 277
Db 285 DAPVAPGRSPLATTVVDFTHVPLPLNHALLAARTQLLEGSDYGGAAAQVPPAPRGS 344
QY 278 PPAVR-PTPCAPLAECKGLLDDSGAKSTED-TAEYSPPKGYTKGLGESLGCSSGAAA 335
Db 345 PSAPSPVPVPCGDFPDC---TYPPEGDPKEDGFPVYGEFPQPLKIKEE-----EGTEA 396
QY 336 GSSGTLLEPLTSLYKSGALDEAAVQSRDYNFPLALAGPPPPP--PPHPHARIKLEN 393
Db 397 SRS-----PRPYLL-----AGASAAATFPDFPL---PPRPPAPPSRP----- 430
QY 394 PLDYGSAWAAAAQCRYGLIAS-----LHGAGAAGPGSGS-----PSAAASSSWH 438
Db 431 ---GEA-AVAAPSAAVSPVSSSGSALECILYKAEGAPPTGSGFAPLPCKPPAAS- 481
QY 439 TLTAEGQLYPCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 498
Db 482 -CULLPRKDSLPAAP-----TSSAAPAIY--PPLGLNG--- 509
QY 499 DFTAPDVWPGMV-SRVVPYSPPTCVKSEMPMD-----SYSGPYGDMRLTARDH 549
Db 510 --LPQLGYOAAVLKDSLPOVYD-----PVLNLRPDSEASQSPQYCFDSL----- 552
QY 550 VLPIDYFPQKTCICGDEASGCHYCALTCGSKVFFKRAAGKOKYLACSRNDCTIDK 609
Db 553 -----PQKTCICGDEASGCHYGLVTCGSKVFFKRAAGKOKYLACSRNDCTIDK 603
QY 610 FRKNCPSRLRKCYEAGMTLGARKLKLGNLQEE-----EGEA--SSTTSPTETT--OKL 663
Db 604 IRRKNCPCALRKCQAGMVLGVRKKEKFKNVVRMALDQVALPQSVAFPNESOTLGQRI 663
QY 664 TVSHIEGYEQPIFLNVLEAIEPGVVCAGHNDNQPDSFAALLSLNELGERQLVHVWKA 723
Db 664 TFSNQETQLVPLPLINLLMSIEPDVYVAGHDNTKPDTSLSLLTSLNOLGERQLVSVKWS 723
QY 724 KALPGFRNLHVDDOMAVIOYSWGLMVFAMGWRSTFNVNMRMLYFAPDLVFNVRHKS 783
Db 724 KSLPGFRNLHIDQIITLIQISWLSMVLGWSYKIVSQMQLYFAPDLINLLMSRKL 783
QY 784 MYSQCVVRHLSQEFGLWLTITPQEFCKMALLFSIIPVGLKNQKFFDELWNYIKEL 843
Db 784 FYSCLTLMQIPQEFVKLVQTHREFCLMKVLLINTIPLGLERSQSQFEEMRSYIRELI 843
QY 844 RIACKRNKPTSCRRFYQLTKLDSVQPIARELHQFTDLLIKSHMVSVDFPEMMAEII 903
Db 844 KAIGLRQKGVVPSORFYQLTKLDSLHDLVQLHQLCLNTFIQSRLAVAEFFEMSEVI 903

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Db 713 QGVVANSQRYQLTKLMSHDLVKQLHLFCLNTFLQSRALSVEFEMMSEVIAAQLPK 772  
Qy 910 ILSGKVPPIYFH 921  
Db 773 ILAGWVXPLLFH 784

RESULT 12  
A39596  
progesterone receptor B form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 20-Aug-1999  
C:Accession: A39596; I49111  
R:Schott, D.R.; Shyamala, G.; Schneider, W.; Parry, G.  
Biochemistry 30, 7014-7020, 1991  
A:Title: Molecular cloning, sequence analyses, and expression of complementary DNA encoding the human progesterone receptor B form  
A:Reference number: A39596; MUID:91299759  
A:Accession: A39596  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-923 <SCH>  
A:Cross-references: GB:M68915; GB:J05333; NID:g200471; PIDN:AAA39971.1; PID:g200472  
R:Ragihara, K.; Wu-Peng, X.S.; Funabashi, T.; Kato, J.; Pfaff, D.W.  
Biochem. Biophys. Res. Commun. 205, 1093-1101, 1994  
A:Title: Nucleic acid sequence and DNase hypersensitive sites of the 5' region of the mouse progesterone receptor B form  
A:Reference number: I49111; MUID:95100931  
A:Accession: I49111  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-9 <HAG>  
A:Cross-references: EMBL:U12644; NID:g639916; PIDN:AAA66067.1; PID:g639917  
C:Superfamily: progesterone receptor; erba transforming protein homology  
C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zinc finger  
F:555-819/Domain: erba transforming protein homology <ERBA>  
F:557-577/Region: zinc finger  
F:593-617/Region: zinc finger

Query Match 24.5%; Score 1205; DB 2; Length 923;  
Best Local Similarity 32.2%; Pred. No. 2.1e-50;  
Matches 337; Conservative 119; Mismatches 301; Indels 288; Gaps 36;

Qy 35 QNPGPRHPEAASAAP--GASILLQLQQQQQQQQQQQQQQQQQQQQQQQQQQTSP----- 86  
Db 7 KDOVLHTSGSPPHIGSPLL-----ARLDGPFQGSQSHSDVSVVPIPISLD 57  
Qy 87 -----RQOQQQOQEDGSPQA-----HRRGTGY-----LVID 113  
Db 58 GLLFPRSCRGPELPDCKTGQDQSLSDVEGAFSGVEATHREGGRNRPPEKDSRLDSDVLD 117  
Qy 114 EEQPSQPSQSALECHPERGCVPEPGNAVAASKGLPQQLPAPPDDEDSAPSTLSLGLPTF 173  
Db 118 SLTTPSGPE---QSHAS---PPACEAITSWCLFGPELP-----EDPRVPATKGLLSP-- 164  
Qy 174 PGLSSCSADLKDTLSASTMQLLQOQQQPAVSESSGSRAREASCAPTSSKDNVLLGGTST 233  
Db 165 -----LMSRPEIKVGDSGTGRGQ----- 183  
Qy 234 ISDNKELKAVSVSMGLGVEALEHLSPEQL---RGDCMYAPLIGVPAVPTPCAPLA 290  
Db 184 -----KVLPGK-----LSPPRQLLPTSGSAHPGAGVKPS--PQPA-- 219  
Qy 291 ECKGSLDSDSAGKSTEDTAESYSPFGKGYTKGLESLG---CSGSAAGSGSTLELPSTL 347  
Db 220 ---GEVEEDS-GLETEGSA--SPLLSKSPRALEGTGQGGVAVANAPSAAPGGVTLVPKED 273  
Qy 348 SLXKSGALD-----EAAVQSRDYNNPPL-----A 372  
Db 274 SRSAPVSLQSDSPIAPGRSLPATTWDFIHVPILPLNHALLAARTROLLEGESYDGG 333  
Qy 373 LAGPVPVPPPP-----HPHARIKEN-----PLDYGSAWAAAAAQCVRGDLA 414

Db 334 TAGPCFPPRSPSAPSTVPYRGDFPDCTYPLEGDKEDVEPL-----YGDQ 379  
Qy 415 S-----LHGAGAAGPGSGSP-----SAAASSSHHTLFTAEAGQLYPCPCGGGGGGGG 462  
Db 380 TPGLKIKBEEGADAA---VRSRPRYLTSAGASSSTPDPFLAPAPQAAPSSRSGEAAVAG 436  
Qy 463 GGGGGGGGGGGGA-----GAVAPYGYTRPP-----QGLAGQESD 499  
Db 437 GPSSAAVSPASSSGSALCILYKAEAPTQGSFAPLP-CKPAAASCLLPDRLPLAAPGT 495  
Qy 500 FTAPDVMYPGMVSRVPYPTCVKSEMPWMDSYSGYGMRLTARDHVLPL--IDYFF 557  
Db 496 AAPAIYQPLGL-NGPL-----YQAAVLKDSLFPQVPPYLYNLRL 536  
Qy 558 P-----POKTLICGDEASGCHYGALTGCKVCKVFFKRAAGKOKYLCASR 602  
Db 537 PDEASQSPQYGFDSLQPKICLICGDEASGCHYGVLTCGCKVCKVFFKRAAGKOKYLCASR 596  
Qy 603 NDCITDKFRKNCPCRLRKYCAEAGMTLGARKLKLGNLKLQE--EGEA--SSTTSPTTE 658  
Db 597 NDCIVDKIRKNCPCACLRKCCQAGWVLGGRKFKFNKVRVMRTLDGVALPOSVGLPNES 656  
Qy 659 --TTQKLTVSHTEGTECQDIFLNLEAIEPVGVCAGHDNNQPDFAALLSSNLGERQL 716  
Db 657 QALSQRITFSPNQEIQLVPLPLINLLMSIEPDVIYAGHDNTRKPTDTSLSLTSLNQGERQL 716  
Qy 717 VHVWKAALPGFRNLHVDQMAVIOYSWMLMTFAMGWRFSFTNVNSRMLYFAPDLVFE 776  
Db 717 LSVVWKSLSLPGFRNLHIDDOITLQYSWMSLMVFLGWRYSKHSYKHSYKHSYKHSYKHSY 776  
Qy 777 YRMHKSRYSOCVYRMHLSQEFGLWQITPOEFLCMKALLFSIIPVDGLKNQKFFDELRLM 836  
Db 777 QRMKELSFYSLCTLMQIPEQFVKLQVTHEEFLCMKVLNLLNTIPLGLRSQSQFEEMRS 836  
Qy 837 NYIKELDRITACRKNPTSCSRREYOLTKLDSVQPIARELHOFTDILLIKHMYSDVDP 896  
Db 837 SYIRELKAIGLRQKGVVPTSORFYOLTKLDSLHDLVKQLHLCLNTTIQSKTLAVEFP 896  
Qy 897 EMMAEITISQVPRKILSGKVKPIYFH 921  
Db 897 EMNSEVIAAQLPKILAGWVKPLLFH 921

RESULT 13  
A41401  
mineralocorticoid receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 03-Apr-1992 #sequence\_revision 03-Apr-1992 #text\_change 20-Sep-1999  
C:Accession: A41401  
R:Patel, P.D.; Sherman, T.G.; Goldman, D.J.; Watson, S.J.  
Mol. Endocrinol. 3, 1877-1885, 1989  
A:Title: Molecular cloning of a mineralocorticoid (type I) receptor complementary DNA  
A:Reference number: A41401; MUID:90114194  
A:Accession: A41401  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-981 <PAT>  
A:Cross-references: GB:M36074; NID:g205340; PIDN:AAA41583.1; PID:g205341  
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
C:Keywords: DNA binding; transcription regulation; zinc finger  
F:602-877/Domain: erba transforming protein homology <ERBA>  
F:604-624/Region: zinc finger  
F:640-664/Region: zinc finger

Query Match 22.2%; Score 1092; DB 2; Length 981;  
Best Local Similarity 32.0%; Pred. No. 2.1e-50;  
Matches 310; Conservative 119; Mismatches 306; Indels 234; Gaps 34;

Qy 77 QOQOQOQTSR---QOQOQOQEDGSGPOAHRGRTGYLVLDDEEQPSQPSA----- 124  
Db 121 QOQOQOQSLPTKIYQNMEQLVKYKENGHRSSSTLS--AMSRPLRSFMPDASAASNGGALR 178

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QY 125 -----LECHPERGCVPEP---GAAVAASKGL-----PQQLPAPDEDDNSA 162
Db 179 AIVKSPIICHEKSSSVSPLNMASSVCGVINSMSSTTSFGSPFVHPHPIITQGTSLTCS 238
QY 163 PST-----LSLLGPTFPGLSSCADLKDILSEASTMOLLOQ 198
Db 239 PSVENGRSRSHSPHASNVGSPSSPLSSMKSPISPPSHCS--VKSPVSSPNNVPLRSS 296
QY 199 QOQEA-----VSEGGSGRAREASGAPTSKDNV LGGTSTISDNAKELKAVSVSMG 250
Db 297 VSSPANLNNSRCVSSPSNNTNRRSTLSSTASTVSGIG--SPISNATSYATISGASAG 354
QY 251 LGVLEHLSPG-----EQLRGDCMYAPLLGVPPAVRPTPCAPL-----AECKGSLDD 299
Db 355 ----AIQDVVPSPTDTEKGAHDVFPFKTEVEKATISNGVTGPNIVQYIKSEPDGAFSS 410
QY 300 SAGKSTEDTAEYSPKGGYTKLEGESLGCSSAAAGSGTLELPSTLSLYKSGALDEAA 359
Db 411 CLGNSK-ISPSPFFSVPTKQ---ESSKHSCSGASFKNPTNVNPFPMDSGYFS-FMDD-- 464
QY 360 AYOSRDYNNPLALAGPPPP-----PPPPHPHARIKLENPLDYGSAAWAAAQCRYGDL 413
Db 465 ----KDYLSL-GILGPPVPGDSCEDSAFP---VGIKQEPDDG-----YPE 506
QY 414 ASLHGAGAAGPGSGSPSAASSSWHTLFTAEEGQLYGPCGGGGGGGGGGGGGGGG 473
Db 507 ASIPSSAIVGVNSG-----GQSFHY----- 526
QY 474 GGGEAGAVAPYGYTRPPQGLAQESDFTAPDVWYVPGMVSRVPYSPFCVKSEMPWDS 533
Db 527 ---RIGAQTISLSRSDROGFSQH-----LSSFP-PVNTLVES-----WK-- 562
QY 534 YSPGYGDMLETARDHVLPIDYFP-----POKTLICDGEASGCHYG 576
Db 563 ---PHGD--LSSRRSDGYPVLEYIPENVSSSTLSRVSTGSSRPSKICLVCGDEASGCHYG 617
QY 577 ALTGCGCKVFFKRAAGKOKYLCASRNDCTDKFRKNCPCRLKCYEAGMTLGARKLK 636
Db 618 VVTGCGCKVFFKRAVEGQHNYLCAGRNDCTIDKIRKNCPCARLQKLOAGMNLGARKSK 677
QY 637 KLGNLK-LQEE-----GEASSTTSPTTEET-----QKLTVSHIEGYECQP 675
Db 678 KLGLKLGLHEEQPQPPPPQSPPEGTYIAPTKEFSVNSALVPQLTSTITH-----ALTP 733
QY 676 IFNLVLEALEPGVVCAGHDNNQPSFAALLSSNLGELQVLHVVKWAKALPGFNLHVD 735
Db 734 SPAMTILENTEPTVYAGYDNSKPDPTAESSLTLNRLAAKQMIQVVKWAKVLPGFKNLPLE 793
QY 736 DQMAVIOYSWMLGMVFMAGWRSFTNVNSRMLYFAPDLVFNEMRHKSMYSQCVRRHLS 795
Db 794 DOITLIQYSWMLCSFALSWSRYKHTNSQLLYFAPDLVFNEMRHKSMYSQCVRRHLS 853
QY 796 QFEGWLOITPOEFLCMKALLFTSIPVDGLKNKQFFDELRMNLIKELDRIIACKRNKPTS 855
Db 854 LQFVRLQTLTFEYSIMVKVLLSTVPKDLKSAAFEMRTNVIKELRKMTV---KCPNS 910
QY 856 CS---RREYQTLTKLSDVPTARELHFTFDLLIKSHWSVDPEPMAEIISVQVPKILS 912
Db 911 SQSQWQRYQTLTKLSDMHDVSDLEFCFTTFRESQALKVEFPAMLVEIITDQLEKVES 970
QY 913 GKVRPIYFH 921
Db 971 CNAKPLVYH 979
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RESULT 14  
A29513  
mineralocorticoid receptor - human  
N:Alternate names: aldosterone receptor  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 20-Sep-1999  
C:Accession: A29513  
R:Arriza, J.L.; Weinberger, C.; Cerelli, G.; Glaser, T.M.; Handelin, B.L.; Housman, D.E.

Science 237, 268-275, 1987  
A:Title: Cloning of human mineralocorticoid receptor complementary DNA: structural an  
A:Reference number: A29513; MUID:87263386  
A:Accession: A29513  
A:Molecule type: mRNA  
A:Residues: 1-984 <ARR>  
A:Cross-references: GB:M16801; NID:g187460; PTDN:AAA59571.1; PID:g307166  
C:Genetics:  
A:Gene: GDB:MLR  
A:Cross-references: GDB:120188; OMIM:264350  
A:Map position: 4q31-4q31  
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
F:601-880/Domain: erba transforming protein homology <ERBA>  
F:603-623/Region: zinc finger  
F:639-663/Region: zinc finger

Query Match 22.0%; Score 1078.5; DB 2; Length 984;  
Best Local Similarity 32.8%; Pred. No. 1.1e-49;  
Matches 300; Conservative 101; Mismatches 254; Indels 259; Gaps 30;

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QY 98 SPOAHRRGPTGYL-----VLDEEQP-SQPSALECHPERGCVPEP-----GAAVAASK 145
Db 238 SPNAENGRSRSHPAHASNVGSPSSPLSSMKSSISSPPSHCSVKSPVSSPNNTVLRSSV 297
QY 146 GLPQQL-----PAPDEDD-----SAAPSTL-SLLGP-----TFGLSSCSADLKD 185
Db 298 SSPANINNSRCVSSPSNNTNRRSTLSSPAATVSGSICSPVNNAFSYTASGTISAGSSTLRD 357
QY 186 ILSEASTMOLLOQ---QOEAVSEGSSGRA-----REAGAPTSSKDNLYLGGT 231
Db 358 VVPSDTEQKGAQVFPFKTEVEESATISNGVTGQNLIVQYIKPEPDGAFSS---CLGNG 414
QY 232 STISDNAKELKAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPPAVRPTPCAPLAE 291
Db 415 SKINSDS-----SFSVPIQESTKHSCSTSPKGN-----PTVNPFP----- 451
QY 292 CKGSLDDSAKSTEDTAEY--SPFKGGYTKLEGESLGCSSAAAGSGTLELPSTLSL 349
Db 452 ----FMDCSYFSFMDKDYYSLSGILGPPVPVPGDQ---NCEGS----- 487
QY 350 YKSGALDEAAAYQSRDYNNFPLALAGPPPPPPPHPHARIKLENPLDYGSAAWAAAQCR 409
Db 488 -----GFPVGIQEP-----DDGS----- 501
QY 410 YCDLASLHAGAAAGPGSGSPSAASSSWHTLFTAEEGQLYGPCGGGGGGGGGGGGGG 469
Db 502 YYPEASIPSSAIVGVNSG-----GQSFHY----- 525
QY 470 GGGGGGGEAGAVAPYGYTRPPQGLAQESDFTAPDVWYVPGMVSRVPYSPFCVKSEMPG 529
Db 526 -----RIGAQTISLSRSDROGFSQH-----LSSFP-PVNTLVES----- 559
QY 530 WMSYSGPYGDMLETARDHVLPIDYFP-----POKTLICDGEASG 572
Db 560 WKS-----HGD--LSSRRSDGYPVLEYIPENVSSSTLSRVSTGSSRPSKICLVCGDEASG 612
QY 573 CHYCALTCGCKVFFKRAAGKOKYLCASRNDCTIDKFRKNCPCRLKCYEAGMTLGA 632
Db 613 CHYGVTCGCKVFFKRAVEGQHNYLCAGRNDCTIDKIRKNCPCARLQKLOAGMNLGA 672
QY 633 RKLKLGNLK-LQEEGEAS-----TTSPTTEET-----QKLTVSH 667
Db 673 RKSKLKLGLHEEQPQPPPPQSPPEGTYIAPAKEPSVNTALVPQLSTISR 732
QY 668 IEGYECQPIFNLVLEALEPGVVCAGHDNNQPSFAALLSSNLGELQVLHVVKWAKALP 727
Db 733 ----ALTPSPVMVLENTEPEIVVAGYDSSKPDPTAESSLTLNRLAGKQMIQVVKWAKVLP 788
QY 728 GFRLNHYDDQMAVIOYSWMLGMVFMAGWRSFTNVNSRMLYFAPDLVFNEMRHKSMYSQ 787
Db 789 GFKNLPLEDQITLIQYSWMLCSFALSWSRYKHTNSQFLYFAPDLVFNEMRHKSMYEL 848
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Search completed: January 3, 2002, 23:07:40  
Job time: 836 sec

Query Match	21.7%;	Score 1065;	DB 1;	Length 795;
Best Local Similarity	32.0%;	Pred. No. 4.5e-49;		
Genes	110;	Mismatches 268;	Indels 288;	Gaps 35;

20 RGAFQNLFSVR--EVIQNPGRHPPEAASAPPGASLLLL-----QQQQQQQQQQQ 68